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SEQUENCE LISTING

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Silins, Ginters
Grimmond, Sean
Gartside, Michael
Hancock, John

<120> A NOVEL GENE AND USES THEREFOR

<130> 13198

<140> 09/424,458

<141> 2000-03-16

<150> PCT/AU98/00380

<151> 1998-05-22

<160> 111

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Peptide repeat motif in DnaJ homologues.

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<221> UNSURE

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<223> Xaa at position 2,3 can be any amino acid.

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<221> UNSURE

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<223> Xaa at position 5 can be any amino acid.

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<221> UNSURE

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<223> Xaa at position 7 can be any amino acid.

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Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn Val Cys
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Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln Ser Tyr
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ctg caa tgg ctc caa gat agc gac tac aac ccc aat tgc cgc ctg tgc 197
Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg Leu Cys
45 50 55
aac ata ccc ctg gcc agc cga gag acg acc cgc ctt gtc tgc tat gat 245
Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr Asp
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ctc ttt cac tgg gcc tgc ctc aat gaa cgt gct gcc cag cta ccc cga 293
Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
75 80 85
aac acg gca cct gcc ggc tat cag tgc ccc agc tgc aat ggc ccc atc 341
Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ile
90 95 100
ttc ccc cca acc aac ctg gct ggc ccc gtg gcc tcc gca ctg aga gag 389
Phe Pro Pro Thr Asn Leu Ala Gly Pro Val Ala Ser Ala Leu Arg Glu
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Lys Leu Ala Thr Val Asn Trp Ala Arg Ala Gly Leu Gly Leu Pro Leu
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140 145 150

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 Glu Val Asp Ser Ala Ser Ala Ala Pro Ala Phe Tyr Ser Arg Ala Pro
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 cgg ccc cca gct tcc cca ggc cg^g ccc gag cag cac aca gtg atc cac 629
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 Met Gly Asn Pro Glu Pro Leu Thr His Ala Pro Arg Lys Val Tyr Asp
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Glu Arg Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln
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115 120 125

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Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn
145 150 155 160

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165 170 175

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Pro Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr
195 200 205

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Ala	Ala	Ala	Asp	Ser	Asp	Pro	Asn	Leu	Asp	Pro	Leu	Met	Asn	Pro	His
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cca	cgc	ccc	cga	cct	cca	cta	ggc	ctg	tgc	cac	ccg	ctg	cct	gca	gga	143
Pro	Arg	Pro	Arg	Pro	Pro	Leu	Gly	Leu	Cys	His	Pro	Leu	Pro	Ala	Gly	
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aga	cgc	ccg	gtc	ccg	ggc	cg	gtt	agc	ccc	atg	gga	acg	cag	cgc	ctg	191
Arg	Arg	Pro	Val	Pro	Gly	Arg	Val	Ser	Pro	Met	Gly	Thr	Gln	Arg	Leu	
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Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly	
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Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp	
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Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe 305 310 315	
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Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr 320 325 330 335	
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Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly 355 360 365	
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Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu Thr His Ser His 370 375 380	
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Val Ser Pro Glu Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val 385 390 395	
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Glu Trp Thr Ser Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val	
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Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys	
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cac aag cag tgc aag gat cgc ctg tca gtt gag tgt cgg cgc agg gcc	2015
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Gln Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His	
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Arg Gly Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val	
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Glu Asp Gly Val Phe Asp Ile His Leu	
720 725	
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Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys
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Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val Gln
 65 70 75 80

Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu Gly
 85 90 95

Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro
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Ala His Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys
 115 120 125

Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe Asp
 130 135 140

Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu Met
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Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu Leu
 165 170 175

His Ile Tyr Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val
 180 185 190

Lys Thr Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala Glu
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Phe Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala
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Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp Ile
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Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg Asn
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Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His Leu
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Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg Ser
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Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe Asn
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Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr Ala
325 330 335

Pro Gln Arg Ala Leu Val Ile Thr His Phe Val His Val Ala Glu Lys
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385 390 395 400

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Trp Thr Ser Ala Ala Lys Pro Lys Leu Asp Gln Ala Leu Val Val Glu
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 580 585 590
 Cys Ile Ser Arg Glu Glu Met Val Ser Tyr Phe Leu Arg Ser Ser Ser
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 675 680 685
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Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys	
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Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys Ala Leu Leu Asp	
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Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp Ile Asp Ser Val	
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cct acc tac aag tgg aag cg ^g cag gtg act cag cg ^g aac cct gtg gga	673
Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Gly	
125 130 135 140	
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Ile	Leu	Phe	Gln	Asp	Tyr	His	Ser	Phe	Val	Thr	His	Gly	Cys	Thr	Val	
175							180				185					
gac	aac	ccc	gtc	ctg	gag	cgg	ttc	atc	tcc	ctc	ttc	aac	agc	gtc	tca	865
Asp	Asn	Pro	Val	Leu	Glu	Arg	Phe	Ile	Ser	Leu	Phe	Asn	Ser	Val	Ser	
190					195						200					
cag	tgg	gtg	cag	ctc	atg	atc	ctc	agc	aaa	ccc	aca	gcc	ccg	cag	cg	913
Gln	Trp	Val	Gln	Leu	Met	Ile	Leu	Ser	Lys	Pro	Thr	Ala	Pro	Gln	Arg	
205				210					215			220				
gcc	ctg	gtc	atc	aca	cac	ttt	gtc	cac	gtg	g	g	a	g	ctg	cta	961
Ala	Leu	Val	Ile	Thr	His	Phe	Val	His	Val	Ala	Glu	Lys	Leu	Gln		
225					230					235						
ctg	cag	aac	ttc	aac	acg	ctg	atg	gca	gtg	gtc	ggg	ggc	ctg	agc	cac	1009
Leu	Gln	Asn	Phe	Asn	Thr	Leu	Met	Ala	Val	Val	Gly	Gly	Leu	Ser	His	
240				245					250							
agc	tcc	atc	tcc	cgc	ctc	aag	gag	acc	cac	agc	cac	gtt	agc	cct	gag	1057
Ser	Ser	Ile	Ser	Arg	Leu	Lys	Glu	Thr	His	Ser	His	Val	Ser	Pro	Glu	
255					260					265						
acc	atc	aag	ctc	tgg	gag	ggt	ctc	acg	gaa	cta	gtg	acg	g	ca	ggc	1105
Thr	Ile	Lys	Leu	Trp	Glu	Gly	Leu	Thr	Glu	Leu	Val	Thr	Ala	Thr	Gly	
270					275					280						
aac	tat	ggc	aac	tac	cg	cgt	cg	ctg	gca	gcc	tgt	gtg	ggc	ttc	cgc	1153
Asn	Tyr	Gly	Asn	Tyr	Arg	Arg	Arg	Leu	Ala	Ala	Cys	Val	Gly	Phe	Arg	
285					290					295			300			
ttc	ccg	atc	ctg	ggt	gt	cac	ctc	aag	gac	ctg	gtg	gcc	ctg	cag	ctg	1201
Phe	Pro	Ile	Leu	Gly	Val	His	Leu	Lys	Asp	Leu	Val	Ala	Leu	Gln	Leu	
305						310					315					
gca	ctg	cct	gac	tgg	ctg	gac	cca	gcc	cg	acc	cg	ctc	aac	ggg	ggc	1249
Ala	Leu	Pro	Asp	Trp	Leu	Asp	Pro	Ala	Arg	Thr	Arg	Leu	Asn	Gly	Ala	
320						325					330					
aag	atg	aag	cag	ctc	ttt	agc	atc	ctg	gag	gag	ctg	gcc	atg	gtg	acc	1297
Lys	Met	Lys	Gln	Leu	Phe	Ser	Ile	Leu	Glu	Glu	Leu	Ala	Met	Val	Thr	
335					340					345						

agc	ctg	cgg	cca	cca	gta	cag	gcc	aac	ccc	gac	ctg	ctg	agc	ctg	ctc	1345
Ser	Leu	Arg	Pro	Pro	Val	Gln	Ala	Asn	Pro	Asp	Leu	Leu	Ser	Leu	Leu	
350						355					360					
acg	gtg	tct	ctg	gat	cag	tat	cag	acg	gag	gat	gag	ctg	tac	cag	ctg	1393
Thr	Val	Ser	Leu	Asp	Gln	Tyr	Gln	Thr	Glu	Asp	Glu	Leu	Tyr	Gln	Leu	
365						370					375				380	
tcc	ctg	cag	cgg	gag	ccg	cgc	tcc	aag	tcc	tcg	cca	acc	agc	ccc	acg	1441
Ser	Leu	Gln	Arg	Glu	Pro	Arg	Ser	Lys	Ser	Ser	Pro	Thr	Ser	Pro	Thr	
385								390					395			
agt	tgc	acc	cca	cca	ccc	cgg	ccc	ccg	gta	ctg	gag	gag	tgg	acc	tcg	1489
Ser	Cys	Thr	Pro	Pro	Pro	Arg	Pro	Pro	Val	Leu	Glu	Glu	Trp	Thr	Ser	
400								405					410			
gct	gcc	aaa	ccc	aag	ctg	gat	cag	gcc	ctc	gtg	gtg	gag	cac	atc	gag	1537
Ala	Ala	Lys	Pro	Lys	Leu	Asp	Gln	Ala	Leu	Val	Val	Glu	His	Ile	Glu	
415								420					425			
aag	atg	gtg	gag	tct	gtg	ttc	cg	aac	ttt	gac	gtc	gat	ggg	gat	ggc	1585
Lys	Met	Val	Glu	Ser	Val	Phe	Arg	Asn	Phe	Asp	Val	Asp	Gly	Asp	Gly	
430								435					440			
cac	atc	tca	cag	gaa	ttc	cag	atc	atc	cgt	ggg	aac	ttc	cct	tac		1633
His	Ile	Ser	Gln	Glu	Glu	Phe	Gln	Ile	Ile	Arg	Gly	Asn	Phe	Pro	Tyr	
445								450					455			460
ctc	agc	gcc	ttt	ggg	gac	ctc	gac	cag	aac	cag	gat	ggc	tgc	atc	agc	1681
Leu	Ser	Ala	Phe	Gly	Asp	Leu	Asp	Gln	Asn	Gln	Asp	Gly	Cys	Ile	Ser	
465									470					475		
agg	gag	gag	atg	gtt	tcc	tat	ttc	ctg	cgc	tcc	agc	tct	gtg	ttg	ggg	1729
Arg	Glu	Glu	Met	Val	Ser	Tyr	Phe	Leu	Arg	Ser	Ser	Ser	Val	Leu	Gly	
480									485					490		
ggg	cgc	atg	ggc	ttc	gta	cac	aac	ttc	cag	gag	agc	aac	tcc	ttg	cgc	1777
Gly	Arg	Met	Gly	Phe	Val	His	Asn	Phe	Gln	Glu	Ser	Asn	Ser	Leu	Arg	
495									500					505		
ccc	gtc	gcc	tgc	cgc	cac	tgc	aaa	gcc	ctg	atc	ctg	ggc	atc	tac	aag	1825
Pro	Val	Ala	Cys	Arg	His	Cys	Lys	Ala	Leu	Ile	Leu	Gly	Ile	Tyr	Lys	
510									515					520		

cag ggc ctc aaa tgc cga gcc tgt gga gtg aac tgc cac aag cag tgc 1873
 Gln Gly Leu Lys Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys
 525 530 535 540
 aag gat cgc ctg tca gtt gag tgt cgg cgc agg gcc cag agt gtg agc 1921
 Lys Asp Arg Leu Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser
 545 550 555
 ctg gag ggg tct gca ccc tca ccc tca ccc atg cac agc cac cat cac 1969
 Leu Glu Gly Ser Ala Pro Ser Pro Ser Pro Met His Ser His His His
 560 565 570
 cgc gcc ttc agc ttc tct ctg ccc cgc cct ggc agg cga ggc tcc agg 2017
 Arg Ala Phe Ser Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg
 575 580 585
 cct cca gag atc cgt gag gag gag gta cag acg gtg gag gat ggg gtg 2065
 Pro Pro Glu Ile Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val
 590 595 600
 ttt gac atc cac ttg taatagatgc tgtgggttggaa tcaaggactc attcctgcct 2120
 Phe Asp Ile His Leu
 605
 tggagaaaat acttcaacca gagcagggag cctgggggtg tcggggcagg aggctggga 2180
 tggttgtggg atatgagggt ggcattgcagc tgagggcagg gccaggctg gtgtccctaa 2240
 gggtgtacag actcttgtga atatttgtat tttccagatg gaataaaaag gcccgtgtaa 2300
 ttaacccttc 2309

<210> 7
 <211> 609
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu
 1 5 10 15
 Leu Arg Gly Cys Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp
 20 25 30

Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro
 35 40 45

 Ser Ser Gln Leu Ala Ala Lys Leu Leu His Ile Tyr Gln Gln Ser Arg
 50 55 60

 Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg
 65 70 75 80

 Tyr Trp Ile Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu
 85 90 95

 Ala Glu Gln Ile Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn
 100 105 110

 Arg Arg His Ser Ser Leu Ile Asp Ile Asp Ser Val Pro Thr Tyr Lys
 115 120 125

 Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Gly Gln Lys Lys Arg
 130 135 140

 Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu
 145 150 155 160

 His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln
 165 170 175

 Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val
 180 185 190

 Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln
 195 200 205

 Leu Met Ile Leu Ser Lys Pro Thr Ala Pro Gln Arg Ala Leu Val Ile
 210 215 220

 Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe
 225 230 235 240

 Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser
 245 250 255

 Arg Leu Lys Glu Thr His Ser His Val Ser Pro Glu Thr Ile Lys Leu
 260 265 270

 Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Gly Asn
 275 280 285

 Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu
 290 295 300

 Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp
 305 310 315 320

 Trp Leu Asp Pro Ala Arg Thr Arg Leu Asn Gly Ala Lys Met Lys Gln
 325 330 335

Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro
340 345 350

Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu
355 360 365

Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg
370 375 380

Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro
385 390 395 400

Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Ala Ala Lys Pro
405 410 415

Lys Leu Asp Gln Ala Leu Val Val Glu His Ile Glu Lys Met Val Glu
420 425 430

Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln
435 440 445

Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe
450 455 460

Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
465 470 475 480

Val Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly
485 490 495

Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys
500 505 510

Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys
515 520 525

Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu
530 535 540

Ser Val Glu Cys Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser
545 550 555 560

Ala Pro Ser Pro Ser Pro Met His Ser His His His Arg Ala Phe Ser
565 570 575

Phe Ser Leu Pro Arg Pro Gly Arg Arg Gly Ser Arg Pro Pro Glu Ile
580 585 590

Arg Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His
595 600 605

Leu

<210> 8
<211> 832
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (11)..(733)

<400> 8
gccccggccatg ccg ccc tta ctg ccc ctg cgc ctg tgc cggttgg 49
Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp
1 5 10

ccc cgc aac cct ccc tcc cgg ctc ctc gga gcg gcc gcc ggg cag cgg 97
Pro Arg Asn Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala Gly Gln Arg
15 20 25

tcc aga ccc agt act tat tat gaa ctg ttg ggg gtg cat cct ggt gcc 145
Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala
30 35 40 45

agc act gag gaa gtt aaa cga gct ttc ttc tcc aag tcc aaa gag ctg 193
Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu
50 55 60

cac cca gac cgg gac cct ggg aac cca agc ctg cac agc cgc ttt gtg 241
His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val
65 70 75

gag ctg agc gag gca tac cgt gtg ctc agc cgt gag cag agc cgc cgc 289
Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg
80 85 90

agc tat gat gac cag ctc cgc tca ggt agt ccc cca aag tct cca cga 337
Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg
95 100 105

acc aca gtc cat gac aag tct gcc cac caa aca cac agc tcc tgg aca 385
Thr Thr Val His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr
110 115 120 125

ccc ccc aac gca cag tac tgg tcc cag ttt cac agc gtg agg cca cag 433
Pro Pro Asn Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln
130 135 140

ggg ccc cag ttg agg cag cag caa cac aaa caa aac aaa caa gtg ctg	481
Gly Pro Gln Leu Arg Gln Gln His Lys Gln Asn Lys Gln Val Leu	
145 150 155	
ggg tac tgc ctc ctc ctc atg ctg gcg ggc atg ggc ctg cac tac att	529
Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile	
160 165 170	
gcc ttc agg aag gtg aag cag atg cac ctt aac ttc atg gat gaa aag	577
Ala Phe Arg Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys	
175 180 185	
gat cggttccatcaca gcc ttc tac aac gaa gcc cggttccatcaca gcc agg	625
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg	
190 195 200 205	
gcc aac aga ggc atc ctt cag cag gag cga caa cggttccatcaca ggg cag cggttccatcaca	673
Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg	
210 215 220	
cag ccg cca cca tcc gag cca acc caa ggc ccc gag atc gtg ccc cggttccatcaca	721
Gln Pro Pro Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg	
225 230 235	
ggc gcc ggc ccc tgaggggctc acctggatgg ggctgcagt gcgttccatcaca	773
Gly Ala Gly Pro	
240	
tttgcttcct tccctggacg gcccgcctccc cgaaacgcgc gcaataaaagt gattcgcag	832

<210> 9
<211> 241
<212> PRT
<213> Homo sapiens

<400> 9	
Met Pro Pro Leu Leu Pro Leu Arg Leu Cys Arg Leu Trp Pro Arg Asn	
1 5 10 15	
Pro Pro Ser Arg Leu Leu Gly Ala Ala Ala Gly Gln Arg Ser Arg Pro	
20 25 30	
Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu	
35 40 45	
Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp	
50 55 60	

Arg Asp Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser
65 70 75 80

Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp
85 90 95

Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys Ser Pro Arg Thr Thr Val
100 105 110

His Asp Lys Ser Ala His Gln Thr His Ser Ser Trp Thr Pro Pro Asn
115 120 125

Ala Gln Tyr Trp Ser Gln Phe His Ser Val Arg Pro Gln Gly Pro Gln
130 135 140

Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val Leu Gly Tyr Cys
145 150 155 160

Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg
165 170 175

Lys Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile
180 185 190

Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Asn Arg
195 200 205

Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu Gly Gln Arg Gln Pro Pro
210 215 220

Pro Ser Glu Pro Thr Gln Gly Pro Glu Ile Val Pro Arg Gly Ala Gly
225 230 235 240

Pro

<210> 10

<211> 13

<212> PRT

<213> C. elegans

<400> 10

Asp Val Asp Glu Glu Asp Glu Val Glu Asp Ile Glu Phe
1 5 10

<210> 11

<211> 13

<212> PRT

<213> Homo sapiens

<400> 11

Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe
1 5 10

<210> 12
<211> 13
<212> PRT
<213> C. elegans

<400> 12
Asp His Asp Arg Asp Gly Phe Ile Ser Gln Glu Glu Phe
1 5 10

<210> 13
<211> 13
<212> PRT
<213> Homo sapiens

<400> 13
Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
1 5 10

<210> 14
<211> 13
<212> PRT
<213> C. elegans

<400> 14
Asp Val Asp Met Asp Gly Gln Ile Ser Lys Asp Glu Leu
1 5 10

<210> 15
<211> 37
<212> PRT
<213> Homo sapiens

<400> 15
His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn
1 5 10 15

Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg
20 25 30

Leu Lys Glu Thr His
35

<210> 16
<211> 37
<212> PRT
<213> C. elegans

<400> 16
Lys Phe Val His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn
1 5 10 15

Thr Leu Met Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg
20 25 30

Leu Ala Lys Thr Tyr
35

<210> 17
<211> 50
<212> PRT
<213> Homo sapiens

<400> 17
His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His
1 5 10 15

Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg
20 25 30

Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val
35 40 45

Glu Cys
50

<210> 18
<211> 50
<212> PRT
<213> C. elegans

<400> 18
His Asn Phe His Glu Thr Thr Phe Leu Thr Pro Thr Thr Cys Asn His
1 5 10 15

Cys Asn Lys Leu Leu Trp Gly Ile Leu Arg Gln Gly Phe Lys Cys Lys
20 25 30

Asp Cys Gly Leu Ala Val His Ser Cys Cys Lys Ser Asn Ala Val Ala
35 40 45

Glu Cys
50

<210> 19
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Nucleotide sequence of pGEX and mcg7 junction.

<400> 19

gggatcccc tggtc

15

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Nucleotide sequence of pGEX and mcg7 junction.

<400> 20
gaattcggca cgagccgacg g

21

<210> 21
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Nucleotide sequence of myc-tag/mcg7 junction.

<400> 21
atggaggaga agctgatctc cgaggaggac ctgcccgggg cagctggatc cgccagccac 60
cccgcgccgg cggccatg 78

<210> 22
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:The amino acid sequence encoded by the nucleotide sequence of SEQ ID NO: 21.

<400> 22
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Pro Gly Ala Ala Gly
1 5 10 15
Ser Ala Ala His Pro Ala Pro Ala Ala Met
20 25

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Nucleotide sequence of pGEX and mcg7 junction.

<400> 23
ggatccgcag cccacccgc gccggcgcc atg

33

<210> 24
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:The amino acid sequence encoded by the nucleotide sequence of SEQ ID NO: 23.

<400> 24
Gly Ser Ala Ala His Pro Ala Pro Ala Ala Met
1 5 10

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-7 specific oligonucleotide.

<400> 25
ggacaaagtg tgtgatgaac c

21

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-7 specific oligonucleotide.

<400> 26
ctcatcctcc gtctgatact g

21

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 27
gttagatgtgg atcagcttgg 20

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 28
aggtggagaa tggtaagg 19

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 29
gtcatagtct gtctcctact 20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 30
acatagacag cgtgcctacc 20

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 31
tacaacctta gggacaccag 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 32
tgctgagcct gctcacggtg 20

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 33
caagtgaaca gcacgtcc 18

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide

<400> 34
gactatctca aggaccagct g 21

<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 35
ggttcggtcc gagcccg 18

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 36
ggagcgatac tccaaagttagg t 21

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 37
agcgggccag gccccttc 18

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 38
catcctggtc caatgcgtc 20

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 39
gcactgagga agttaaacga gc

22

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 40
gctcgttaa cttcctcagt gc

22

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 41
gctcagctcc acaaaaggcggc t

21

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 42
accagctccg ctcaggtag

19

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 43
tccaggagct gtgtgtttgg 20

<210> 44
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 44
ccagtttcac agcgtgagg 19

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mcg-18 specific
oligonucleotide.

<400> 45
cagcatgagg aggaggcag 19

<210> 46
<211> 60
<212> PRT
<213> Homo sapiens

<400> 46
Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys
1 5 10 15

Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His
20 25 30

Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp
35 40 45

Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu
50 55 60

<210> 47
<211> 60
<212> PRT
<213> Mus musculus

<400> 47
Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys
1 5 10 15

Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His
20 25 30

Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp
35 40 45

Tyr Asn Pro Asn Cys Arg Leu Cys Asn Thr Pro Leu
50 55 60

<210> 48
<211> 103
<212> PRT
<213> Homo sapiens

<400> 48
Pro Lys Arg Lys Val Thr Asn Leu Phe Cys Phe Glu His Arg Val Asn
1 5 10 15

Val Cys Glu His Cys Leu Val Ala Asn His Ala Lys Cys Ile Val Gln
20 25 30

Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn Pro Asn Cys Arg
35 40 45

Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys
50 55 60

Tyr Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu
65 70 75 80

Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly
85 90 95

Pro Ile Phe Pro Pro Asn Gln
100

<210> 49
<211> 103
<212> PRT
<213> C. elegans

<220>
<221> UNSURE
<222> (10)
<223> Xaa at position 10 can be any amino acid.

<220>
<221> UNSURE
<222> (21)
<223> Xaa at position 21 can be any amino acid.

<220>
<221> UNSURE
<222> (55)
<223> Xaa at position 55 can be any amino acid.

<220>
<221> UNSURE
<222> (77)
<223> Xaa at position 77 can be any amino acid.

<220>
<221> UNSURE
<222> (87)
<223> Xaa at position 87 can be any amino acid.

<400> 49

Pro Lys Arg Lys Val Thr Asn Leu Phe Xaa Tyr Glu His Arg Val Asn
1 5 10 15

Val Cys Glu Leu Xaa Leu Val Asp Asn His Pro Asn Cys Val Val Gln
20 25 30

Ser Tyr Leu Thr Trp Leu Thr Asp Gln Asp Tyr Asp Pro Asn Cys Ser
35 40 45

Leu Cys Lys Thr Thr Leu Xaa Glu Gly Asp Thr Ile Arg Leu Asn Cys
50 55 60

Leu His Leu Leu His Trp Lys Cys Phe Asp Glu Trp Xaa Gly Asn Phe
65 70 75 80

Pro Asp Thr Thr Ala Pro Xaa Gly Tyr Arg Cys Pro Cys Cys Ser Gln
85 90 95

Glu Val Phe Pro Pro Asp Gln
100

<210> 50
<211> 45
<212> PRT
<213> Homo sapiens

<400> 50

Cys Asn Ile Pro Leu Ala Ser Arg Glu Thr Thr Arg Leu Val Cys Tyr
1 5 10 15

Asp Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro
20 25 30

Arg Asn Thr Ala Pro Ala Gly Tyr Gln Cys Pro Ser Cys
35 40 45

<210> 51
<211> 45
<212> PRT
<213> *C. elegans*

<400> 51
Cys Ser Ile Cys Leu Glu Asn Lys Asn Pro Ser Ala Leu Phe Cys Gly
1 5 10 15

His Leu Phe Cys Trp Thr Cys Ile Gln Glu His Ala Val Ala Ala Thr
20 25 30

Ser Ser Ala Ser Thr Ser Ser Ala Arg Cys Pro Gln Cys
35 40 45

<210> 52
<211> 24
<212> PRT
<213> *Homo sapiens*

<400> 52
Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp Tyr Asn
1 5 10 15

Pro Asn Cys Arg Leu Cys Asn Ile
20

<210> 53
<211> 24
<212> PRT
<213> *Saccharomyces pombe*

<400> 53
Cys Ala Thr Thr Asn Thr Pro Lys Trp Arg Arg Asp Glu Ser Gly Asn
1 5 10 15

Pro Ile Cys Asn Ala Cys Gly Leu
20

<210> 54
<211> 66
<212> PRT
<213> *Homo sapiens*

<400> 54
Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala Pro
1 5 10 15

Ala Phe Tyr Ser Gln Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg Pro
20 25 30

Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr His
35 40 45

Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro Gly
50 55 60

Leu His
65

<210> 55
<211> 66
<212> PRT
<213> *Saccharomyces pombe*

<400> 55
Ala Ser Leu Leu Asn Pro Glu Glu Pro Pro Ser Asn Ser Asp Lys Gln
1 5 10 15

Pro Ser Met Ser Asn Gly Pro Lys Ser Glu Val Ser Pro Ser Gln Ser
20 25 30

Gln Gln Ala Pro Leu Ile Gln Ser Ser Thr Ser Pro Val Ser Leu Gln
35 40 45

Phe Pro Pro Glu Val Gln Gly Ser Asn Val Asp Lys Arg Asn Tyr Ala
50 55 60

Leu Asn
65

<210> 56
<211> 259
<212> DNA
<213> *Homo sapiens*

<400> 56
ggcctccctc tgatcgatga ggtggtgagc ccagagcccg agcccccaa cacgtctgac 60
ttctctgact ggtcttagttt taatgccagc agtaccctg gaccagagga ggttagacagc 120
gcctctgctg ccccagcctt ctacagccag gccccccggc ccccagcttc cccaggccgg 180
cccgagcagc acacagtgtat ccacatgggc aatcctgagc ctttgactca cgccccctagg 240
aaggtgtatg atacgcggg 259

<210> 57
<211> 259

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<212> DNA
<213> Homo sapiens

<400> 57
gggctccctc tgatcgatga ggtgataagc ccagagcccc agcccctcaa ttcctcagac 60
ttctctgatt ggtccagctt taatgccacc accacctctg tgcaagagga gagagccagc 120
actccatctg cacctgcttt ctatagccag gctccccgcc ctactccctc cccaaaggcgt 180
cccgagcagc acacagtcat acacatgggg agtactgaag ccctggcaca cgccccaaagg 240
aaagtatatg acacaccgg                                         259

<210> 58
<211> 55
<212> DNA
<213> Homo sapiens

<400> 58
gcactgagag agaagctggc cacagtcaac tggggccggg caggactggg cctcc      55

<210> 59
<211> 55
<212> DNA
<213> Homo sapiens

<400> 59
gcactgagag aaaagcttagc cacagtcaac ttggggccggg caggactggg ctccc      55

<210> 60
<211> 44
<212> DNA
<213> Homo sapiens

<400> 60
gccttgggtt ggctggcccg gctgctaagg agccgggctg ggtc                         44

<210> 61
<211> 44
<212> DNA
<213> Homo sapiens

<400> 61
gctctgggct ggctggccca gctgctcagg agccgggctg ggtc                         44

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<210> 62
<211> 35
<212> DNA
<213> Homo sapiens

<400> 62
ggagactgtg acgatgacaa gtaccgacgt cggcc 35

<210> 63
<211> 35
<212> DNA
<213> Homo sapiens

<400> 63
ggagactgtg atgatgacaa ataccgccgc cggcc 35

<210> 64
<211> 32
<212> DNA
<213> Homo sapiens

<400> 64
cgggatgatg accggacacc aggcctccat gg 32

<210> 65
<211> 32
<212> DNA
<213> Homo sapiens

<400> 65
cgggatgatg accggacagc aggcatccat gg 32

<210> 66
<211> 190
<212> DNA
<213> Homo sapiens

<400> 66
cgtctgactt ctctgactgg tctagttta atgccagcag taccctggc ccagaggagg 60
tagacagcgc ctctgctgcc ccagccttct acagccaggc cccccggccc ccagcttccc 120
caggccggcc cgagcagcac acagtgatcc acatgggcaa tcctgagccc ttgactcacg 180
ccccttaggaa 190

<210> 67
<211> 190
<212> DNA
<213> Homo sapiens

<400> 67
cctcagactt ctctgattgg tccagcttta atgccaccac cacctctgtg caagaggaga 60
gagccagcac tccatctgcg cctgcttct atagccaggc tccccggccct cctccctccc 120
caagccgtcc cgagcagcac acagtcatac acatggggag tactgaagcc ctggcacacg 180
ccccaaaggaa 190

<210> 68
<211> 98
<212> DNA
<213> Homo sapiens

<400> 68
gcactgagag agaagctggc cacagtcaac tgggcccggg caggactggg cctccctctg 60
atcgatgagg tggtgagccc agagccccgag cccctcaa 98

<210> 69
<211> 98
<212> DNA
<213> Homo sapiens

<400> 69
gcactgagag acaagcttagc cacagtcaac tgggcccggg caggactggg cctccctctg 60
atcgatgagg tgataagccc agagccccgag cccctcaa 98

<210> 70
<211> 60
<212> DNA
<213> Homo sapiens

<400> 70
gggatgatga ccggacaccca ggcctccatg gagactgtga cgatgacaag taccgacgtc 60

<210> 71
<211> 60
<212> DNA
<213> Homo sapiens

<400> 71

ggatttatgtga ccggacagca ggcattcatg gagactgtga ttagtacaaa taccggcc 60

<210> 72

<211> 75

<212> DNA

<213> Homo sapiens

<400> 72

taccggccctt cgaaaccagt gcagcggccg atcagtaaac acagagactg gggatcgatc 60

atggggcttt gtaag

75

<210> 73

<211> 74

<212> DNA

<213> Mus musculus

<400> 73

cttccgcgtt tttcattacc gtacgcaccg gtcacgatcg gcatcgccga ggatcggtca 60

tgggactttg caag

74

<210> 74

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc finger consensus.

<220>

<221> UNSURE

<222> (2)..(3)

<223> Xaa at position 2 and 3 can be any amino acid.

<220>

<221> UNSURE

<222> (5)..(8)

<223> Xaa at position 5, 6, 7 and 8 can be any amino acid.

<220>

<221> UNSURE

<222> (10)..(11)

<223> Xaa at position 10 and 11 can be any amino acid.

<220>

<221> UNSURE

<222> (13)..(16)

<223> Xaa at position 13, 14, 15 and 16 can be any amino acid.

<220>

<221> UNSURE

<222> (18)..(37)

<223> Xaa at position 18-37 can be any amino acid.

<220>

<221> UNSURE

<222> (39)..(40)

<223> Xaa at position 39 and 40 can be any amino acid.

<220>

<221> UNSURE

<222> (42)..(59)

<223> Xaa at position 42-59 can be any amino acid.

<220>

<221> UNSURE

<222> (61)..(62)

<223> Xaa at position 61 and 62 can be any amino acid.

<220>

<221> UNSURE

<222> (64)..(81)

<223> Xaa at position 64-81 can be any amino acid.

<220>

<221> UNSURE

<222> (83)..(84)

<223> Xaa at position 83 and 84 can be any amino acid.

<400> 74

Cys Xaa Xaa His Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

His Xaa Xaa Cys Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa
50 55 60

Xaa
65 70 75 80

Xaa Cys Xaa Xaa Cys
85

<210> 75

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Leucine zipper finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>

<221> UNSURE

<222> (9)..(14)

<223> Xaa at position 9-14 can be any amino acid.

<220>

<221> UNSURE

<222> (16)..(21)

<223> Xaa at position 16-21 can be any amino acid.

<220>

<221> UNSURE

<222> (23)..(28)

<223> Xaa at position 23-28 can be any amino acid.

<400> 75

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Arg Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
20 25

<210> 76

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Novel leucine zipper finger consensus.

<220>

<221> UNSURE

<222> (2)..(7)

<223> Xaa at position 2-7 can be any amino acid.

<220>

<221> UNSURE

<222> (9)

<223> Xaa at position 9 can be any amino acid.

<220>

<221> UNSURE

<222> (11)..(16)

<223> Xaa at position 11-16 can be any amino acid.

<220>

<221> UNSURE

<222> (18)

<223> Xaa at position 18 can be any amino acid.

<220>

<221> UNSURE

<222> (20)..(25)

<223> Xaa at position 20-25 can be any amino acid.

<400> 76

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Leu Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
20 25

<210> 77

<211> 627

<212> PRT

<213> C. elegans

<400> 77

Met Ser Ser Lys Val Glu Glu Asp Gln His Gln Glu Leu Leu Thr Glu
1 5 10 15

Asp Gln Leu Val Ala Arg Cys Val Glu Cys Phe Asp Val Asp Glu Glu
20 25 30

Asp Glu Val Glu Asp Ile Glu Phe Val Asp Ala Leu Phe Leu Ser His
35 40 45

Gln Trp Leu Ser Asp Ser Leu Ser Leu Ile Thr His Phe Val Asn Phe
50 55 60

Tyr Gln Glu Thr Arg Asn Val Glu Gln Arg Glu Ala Val Cys Arg Ala
65 70 75 80

Val Ser Phe Trp Ile Glu Lys Phe Pro Met His Phe Asp Ala Gln Pro
85 90 95

Gln Val Cys Ala Gln Val Val Arg Leu Lys Thr Ile Ala Glu Asp Ile
100 105 110

Asn Glu Asn Ile Arg Asn Gly Leu Asp Val Ser Ala Leu Pro Ser Phe
115 120 125

Ala Trp Leu Arg Ala Val Ser Val Arg Asn Pro Leu Ala Lys Gln Thr
130 135 140

Ile Val Arg Val Asp Phe Glu Thr Leu Pro Thr Pro Gly Thr Pro Pro
145 150 155 160

Pro Phe Pro Ile Ala Ser Lys Lys Phe Ser Leu Thr Ala Phe Ser Leu
 165 170 175
 Ser Phe Val Ala Gln Ser Pro Ser Asp Ile Ser Thr Ser Leu Ser His
 180 185 190
 Ile Asp Tyr Arg Val Leu Ser Thr Ile Ser Ile Thr Glu Leu Lys Gln
 195 200 205
 Tyr Val Lys Asp Gly His Leu Arg Ser Cys Pro Met Leu Glu Arg Ser
 210 215 220
 Ile Ser Val Phe Asn Asn Leu Ser Asn Trp Val Gln Cys Leu Ile Leu
 225 230 235 240
 Asn Lys Thr Thr Pro Lys Glu Arg Ala Glu Ile Leu Val Lys Phe Val
 245 250 255
 His Val Ala Lys His Leu Arg Lys Ile Asn Asn Phe Asn Thr Leu Met
 260 265 270
 Ser Val Val Gly Gly Ile Thr His Ser Ser Val Ala Arg Leu Ala Lys
 275 280 285
 Thr Tyr Ala Val Leu Ser Asn Asp Ile Lys Lys Glu Leu Thr Gln Leu
 290 295 300
 Thr Asn Leu Leu Ser Ala Gln His Asn Phe Cys Glu Tyr Arg Lys Ala
 305 310 315 320
 Leu Gly Ala Cys Asn Lys Lys Phe Arg Ile Pro Ile Ile Gly Val His
 325 330 335
 Leu Lys Asp Leu Val Ala Ile Asn Cys Ser Gly Ala Asn Phe Glu Lys
 340 345 350
 Thr Lys Cys Ile Ser Ser Asp Lys Leu Val Lys Leu Ser Lys Leu Leu
 355 360 365
 Ser Asn Phe Leu Val Phe Asn Gln Lys Gly His Asn Leu Pro Glu Met
 370 375 380
 Asn Met Asp Leu Ile Asn Thr Leu Lys Val Ser Leu Asp Ile Arg Tyr
 385 390 395 400
 Asn Asp Asp Asp Ile Tyr Glu Leu Ser Leu Arg Arg Glu Pro Lys Thr
 405 410 415
 Phe Met Asn Phe Glu Pro Ser Arg Gly Leu Val Phe Ala Glu Trp Ala
 420 425 430
 Ser Gly Val Thr Val Ala Pro Asp Asn Ala Thr Val Ser Lys His Ile
 435 440 445
 Ser Ala Met Val Asp Ala Val Phe Lys His Tyr Asp His Asp Arg Asp
 450 455 460

Gly Phe Ile Ser Gln Glu Glu Phe Gln Leu Ile Ala Gly Asn Phe Pro
465 470 475 480

Phe Ile Asp Ala Phe Val Asn Ile Asp Val Asp Met Asp Gly Gln Ile
485 490 495

Ser Lys Asp Glu Leu Lys Thr Tyr Phe Met Ala Ala Asn Lys Asn Thr
500 505 510

Lys Asp Leu Arg Arg Gly Phe Lys His Asn Phe His Glu Thr Thr Phe
515 520 525

Leu Thr Pro Thr Thr Cys Asn His Cys Asn Lys Leu Leu Trp Gly Ile
530 535 540

Leu Arg Gln Gly Phe Lys Cys Lys Asp Cys Gly Leu Ala Val His Ser
545 550 555 560

Cys Cys Lys Ser Asn Ala Val Ala Glu Cys Arg Arg Lys Ser Ser Ser
565 570 575

Asn Leu Thr Arg Ala Ala Glu Trp Phe Ala Ser Pro Arg Gly Ser Met
580 585 590

Arg Ser Arg Ile Ile Asn Thr Cys Asn Asn Ser Gly Ser Thr Pro Asp
595 600 605

Glu Glu Ile Gly Leu Val Ser Leu Ala Cys Glu Glu Val Phe Glu Asp
610 615 620

Asp Asp Leu
625

<210> 78
<211> 530
<212> DNA
<213> Mus musculus

<400> 78
gggatcagag gctgagctgg ttcaagtcaa cagaaaggta tggaggtga actgcattcg 60
ggtttgcatt ctgaagtaaa ggacttgggg gtacgaatcg agcactgtgg gaggctctga 120
gagggttaact tgggtcttag cccacctggc accggcagcc atggcgagca ctctggacct 180
ggacaagggt tgcccgtgga ggagctgctc cgtggctgta tcgaagcctt tgatgactct 240
ggaaagggtgc gagatccaca gctagtgcgc atgttctca tgatgcaccc ctgg tacata 300
ccttcctctc agctggcttc gaaactgctc cacttctatc agcaatcccc gaaggacaac 360
tccaattctc tacagatgaa aacgtgtcac ttggtcaggt actggatctc agccttccca 420
gcagagttcg acttgaaccc agagctggct gaacagatca aggagctgaa ggctctgtta 480

gaccaagaag ggaaccgcag gcacagcagc ctcatcgaca tcgagagtgt 530

<210> 79
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (90)..(719)

<400> 79
cacgcctcg aaggaggtt tgggtcggt ggttcacag tgagtgtgtc tgaagccaaa 60

tggtcggaaa ccgttacccg ctctcctag gcc cggtt cta gtg ggg acc cca acc 113

Ala Arg Leu Val Gly Thr Pro Thr
1 5

gcc tgc ggc tgc ccc tcc caa gtt cct ccc tgt tgg cca ggc atc cag 161

Ala Cys Gly Cys Pro Ser Gln Val Pro Pro Cys Trp Pro Gly Ile Gln
10 15 20

gtc tcc agt ctc cga gct gcg gag aac cca ccg cca cat gct gcc 209

Val Ser Ser Leu Arg Ala Ala Glu Asn Pro Pro His Ala Ala Ala
25 30 35 40

cct ttc cat tcg acc ctg tgg gga gcc agg ctt ccg ggg ccc cgt tcc 257

Pro Phe His Ser Thr Leu Trp Gly Ala Arg Leu Pro Gly Pro Arg Ser
45 50 55

tcc tgt gtg aac tgg gcc ccc cgc ccc cat tcc cag aca tca agg ccg 305

Ser Cys Val Asn Trp Ala Pro Arg Pro His Ser Gln Thr Ser Arg Pro
60 65 70

cgt ctc cag ata gcc acg att tca ttc ctc gct ccc cac agg tcc ctc 353

Arg Leu Gln Ile Ala Thr Ile Ser Phe Leu Ala Pro His Arg Ser Leu
75 80 85

tcc cca aaa tat tcc cat ctt gtc cta gcc cat ccc cca gac tat ctc 401

Ser Pro Lys Tyr Ser His Leu Val Leu Ala His Pro Pro Asp Tyr Leu
90 95 100

aag gac cag ctg tcc cca cgc ccc cga cct cca cta ggc ctg tgc cac 449

Lys Asp Gln Leu Ser Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His
105 110 115 120

ccg ctg cct gca gga aga cgc ccg gtc ccg ggc cggtt agc ccc atg	497
Pro Leu Pro Ala Gly Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met	
125 130 135	
gga acg cag cgc ctg tgt ggc cgc ggg act caa ggc tgg cct ggc tca	545
Gly Thr Gln Arg Leu Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser	
140 145 150	
agt gaa cag cac gtc cag gag gcg acc tcg tcc gcg ggt ttg cat tct	593
Ser Glu Gln His Val Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser	
155 160 165	
ggg gtg gac gag ctg ggg gtt cgg tcc gag ccc ggt ggg agg ctc ccg	641
Gly Val Asp Glu Leu Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro	
170 175 180	
gag cgc agc ctg ggc cca gcc cac ccc gcg ccg gcg gcc atg gca ggc	689
Glu Arg Ser Leu Gly Pro Ala His Pro Ala Pro Ala Ala Met Ala Gly	
185 190 195 200	
acc ctg gac ctg gac aag ggc tgc acg gtg g	720
Thr Leu Asp Leu Asp Lys Gly Cys Thr Val	
205 210	
<210> 80	
<211> 210	
<212> PRT	
<213> Homo sapiens	
<400> 80	
Ala Arg Leu Val Gly Thr Pro Thr Ala Cys Gly Cys Pro Ser Gln Val	
1 5 10 15	
Pro Pro Cys Trp Pro Gly Ile Gln Val Ser Ser Leu Arg Ala Ala Glu	
20 25 30	
Asn Pro Pro Pro His Ala Ala Ala Pro Phe His Ser Thr Leu Trp Gly	
35 40 45	
Ala Arg Leu Pro Gly Pro Arg Ser Ser Cys Val Asn Trp Ala Pro Arg	
50 55 60	
Pro His Ser Gln Thr Ser Arg Pro Arg Leu Gln Ile Ala Thr Ile Ser	
65 70 75 80	
Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser His Leu Val	
85 90 95	

Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser Pro Arg Pro
100 105 110

Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly Arg Arg Pro
115 120 125

Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu Cys Gly Arg
130 135 140

Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val Gln Glu Ala
145 150 155 160

Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu Gly Val Arg
165 170 175

Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly Pro Ala His
180 185 190

Pro Ala Pro Ala Ala Met Ala Gly Thr Leu Asp Leu Asp Lys Gly Cys
195 200 205

Thr Val
210

<210> 81

<211> 61

<212> PRT

<213> Homo sapiens

<400> 81

Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val
1 5 10 15

Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp
20 25 30

Pro Gly Asn Pro Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala
35 40 45

Tyr Arg Val Leu Ser Arg Glu Ser Arg Arg Ser Tyr Asp
50 55 60

<210> 82

<211> 62

<212> PRT

<213> C. elegans

<400> 82

Tyr Tyr Glu Ile Leu Gly Val Ser Lys Thr Ala Glu Glu Arg Glu Ile
1 5 10 15

Arg Lys Ala Tyr Lys Arg Leu Ala Met Lys Tyr His Pro Asp Arg Asn
20 25 30

Gln Gly Asp Lys Glu Ala Glu Ala Lys Phe Lys Glu Ile Lys Glu Ala
35 40 45

Tyr Glu Val Leu Thr Asp Ser Gln Lys Arg Ala Ala Tyr Asp
50 55 60

<210> 83

<211> 37

<212> PRT

<213> Homo sapiens

<400> 83

Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val His Pro
1 5 10 15

Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys Ser Lys
20 25 30

Glu Leu His Pro Asp
35

<210> 84

<211> 37

<212> PRT

<213> C. elegans

<400> 84

Lys Lys Ile Arg Gln Arg Thr His Tyr Glu Val Leu Gly Val Glu Ser
1 5 10 15

Thr Ala Thr Leu Ser Glu Ile Lys Ser Ala Phe Tyr Ala Gln Ser Lys
20 25 30

Lys Val His Pro Asp
35

<210> 85

<211> 32

<212> PRT

<213> Homo sapiens

<400> 85

Ser Leu His Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu
1 5 10 15

Ser Arg Glu Gln Ser Arg Arg Ser Tyr Asp Asp Gln Leu Arg Ser Gly
20 25 30

<210> 86
<211> 32
<212> PRT
<213> C. elegans

<400> 86
Ser Ala Thr Ala Ser Phe Leu Glu Leu Lys Asn Ala Tyr Asp Val Leu
1 5 10 15
Arg Arg Pro Ala Asp Arg Arg Leu Tyr Asp Tyr Gln Leu Arg Gly Gly
20 25 30

<210> 87
<211> 42
<212> PRT
<213> Homo sapiens

<400> 87
Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr Ile Ala Phe Arg Lys
1 5 10 15
Val Lys Gln Met His Leu Asn Phe Met Asp Glu Lys Asp Arg Ile Ile
20 25 30
Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg
35 40

<210> 88
<211> 42
<212> PRT
<213> C. elegans

<400> 88
Leu Val Leu Val Ala Gly Tyr Asn Gly Gly Tyr Leu Tyr Leu Leu Ala
1 5 10 15
Tyr Asn Gln Lys Gln Leu Asp Lys Leu Ile Asp Glu Asp Glu Ile Ala
20 25 30
Lys Cys Phe Leu Arg Gln Lys Glu Phe Arg
35 40

<210> 89
<211> 41
<212> PRT
<213> Homo sapiens

<400> 89
Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val
1 5 10 15

Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp
20 25 30

Pro Gly Asn Pro Ser Leu His Ser Arg
35 40

<210> 90
<211> 41
<212> PRT
<213> C. elegans

<400> 90
Tyr Tyr Glu Ile Ile Gly Val Ser Ala Ser Ala Thr Arg Gln Glu Ile
1 5 10 15

Arg Asp Ala Phe Leu Lys Lys Thr Lys Gln Leu His Pro Asp Gln Ser
20 25 30

Arg Lys Ser Ser Lys Ser Asp Ser Arg
35 40

<210> 91
<211> 22
<212> PRT
<213> Homo sapiens

<400> 91
Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln
1 5 10 15

Ser Arg Arg Ser Tyr Asp
20

<210> 92
<211> 22
<212> PRT
<213> C. elegans

<400> 92
Gln Phe Met Leu Val Lys Glu Ala Tyr Asp Val Leu Arg Asn Glu Glu
1 5 10 15

Lys Arg Lys Glu Tyr Asp
20

<210> 93
<211> 44
<212> PRT
<213> Homo sapiens

<400> 93

Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln Val
1 5 10 15

Leu Gly Tyr Cys Leu Leu Leu Met Leu Ala Gly Met Gly Leu His Tyr
20 25 30

Ile Ala Phe Arg Lys Val Lys Gln Met His Leu Asn
35 40

<210> 94
<211> 44
<212> PRT
<213> C. elegans

<400> 94

Arg Asn Pro Glu Asp Glu Tyr Leu Arg Glu Lys Trp Lys Asn Arg Met
1 5 10 15

Leu Val Val Leu Ala Ala Thr Val Met Ala Leu Ile Gly Ala Asn Ile
20 25 30

Val Tyr Ile Arg Lys Leu Gln Ala Asp Arg Leu Ser
35 40

<210> 95
<211> 36
<212> PRT
<213> Homo sapiens

<400> 95

Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala Ser Thr Glu Glu Val
1 5 10 15

Lys Arg Ala Phe Phe Ser Lys Ser Lys Glu Leu His Pro Asp Arg Asp
20 25 30

Pro Gly Asn Pro
35

<210> 96
<211> 36
<212> PRT
<213> S. pombe

<400> 96

Tyr Tyr Asp Leu Leu Gly Ile Ser Thr Asp Ala Thr Ala Val Asp Ile
1 5 10 15

Lys Lys Ala Tyr Arg Lys Leu Ala Val Lys Tyr His Pro Asp Lys Asn
20 25 30

Pro Asp Asp Pro
35

<210> 97
<211> 40
<212> PRT
<213> Homo sapiens

<400> 97
Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu Gln
1 5 10 15
Ser Arg Arg Ser Tyr Asp Asp Gln Leu Arg Ser Gly Ser Pro Pro Lys
20 25 30
Ser Pro Arg Thr Thr Val His Asp
35 40

<210> 98
<211> 40
<212> PRT
<213> S. pombe

<400> 98
Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln Val Leu Gly Asp Glu Lys
1 5 10 15
Leu Arg Ser Gln Tyr Asp Gln Phe Gly Lys Glu Lys Ala Val Pro Glu
20 25 30
Gln Gly Phe Thr Asp Ala Tyr Asp
35 40

<210> 99
<211> 29
<212> PRT
<213> Homo sapiens

<400> 99
Asp Arg Ile Ile Thr Ala Phe Tyr Asn Glu Ala Arg Ala Arg Ala Arg
1 5 10 15
Ala Asn Arg Gly Ile Leu Gln Gln Glu Arg Gln Arg Leu
20 25

<210> 100
<211> 29
<212> PRT
<213> S. pombe

<400> 100

Asp Arg Lys Lys Asn Ala Gln Ile Arg Glu Arg Glu Ala Leu Ala Lys
1 5 10 15

Arg Glu Gln Glu Met Ile Glu Asp Arg Arg Gln Arg Ile
20 25

<210> 101
<211> 19
<212> PRT
<213> Homo sapiens

<400> 101
Pro Gln Gly Pro Gln Leu Arg Gln Gln Gln His Lys Gln Asn Lys Gln
1 5 10 15

Val Leu Gly

<210> 102
<211> 19
<212> PRT
<213> S. pombe

<400> 102
Pro Gln Gly Ala Ser Glu Lys Phe Gln Lys Ile Ser Glu Ala Tyr Gln
1 5 10 15

Val Leu Gly

<210> 103
<211> 71
<212> PRT
<213> Homo sapiens

<400> 103
Ala Gly Gln Arg Ser Arg Pro Ser Thr Tyr Tyr Glu Leu Leu Gly Val
1 5 10 15

His Pro Gly Ala Ser Thr Glu Glu Val Lys Arg Ala Phe Phe Ser Lys
20 25 30

Ser Lys Glu Leu His Pro Asp Arg Asp Pro Gly Asn Pro Ser Leu His
35 40 45

Ser Arg Phe Val Glu Leu Ser Glu Ala Tyr Arg Val Leu Ser Arg Glu
50 55 60

Gln Ser Arg Arg Ser Tyr Asp
65 70

<210> 104

>
<211> 71
<212> PRT
<213> Drosophila virilis

<400> 104
Ser Ser Ser Arg Met Gln Ala Lys Asp Tyr Tyr Ala Thr Leu Gly Val
1 5 10 15

Ala Lys Asn Ala Asn Ala Lys Asp Ile Lys Lys Ala Tyr Tyr Glu Leu
20 25 30

Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Asp Ala Ser
35 40 45

Lys Lys Phe Gln Asp Val Ser Glu Ala Tyr Glu Val Leu Ser Asp Asp
50 55 60

Gln Lys Arg Arg Glu Tyr Asp
65 70

<210> 105
<211> 397
<212> PRT
<213> Homo sapiens

<400> 105
Met Val Lys Glu Thr Thr Tyr Tyr Asp Val Leu Gly Val Lys Pro Asn
1 5 10 15

Ala Thr Gln Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys
20 25 30

Tyr His Pro Asp Lys Asn Pro Asn Glu Gly Glu Lys Phe Lys Gln Ile
35 40 45

Ser Gln Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Glu Leu Tyr
50 55 60

Asp Lys Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ala Gly Gly Gly
65 70 75 80

Phe Gly Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly
85 90 95

Arg Met Gln Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser
100 105 110

Val Thr Leu Glu Asp Leu Tyr Asn Gly Ala Thr Arg Lys Leu Ala Leu
115 120 125

Gln Lys Asn Val Ile Cys Asp Lys Cys Glu Gly Arg Gly Gly Lys Lys
130 135 140

Gly Ala Val Glu Cys Cys Pro Asn Cys Arg Gly Thr Gly Met Gln Ile
145 150 155 160

Arg Ile His Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Ser Val
 165 170 175

 Cys Met Glu Cys Gln Gly His Gly Glu Arg Ile Ser Pro Lys Asp Arg
 180 185 190

 Cys Lys Ser Cys Asn Gly Arg Lys Ile Val Arg Glu Lys Lys Ile Leu
 195 200 205

 Glu Val His Ile Asp Lys Gly Met Lys Asp Gly Gln Lys Ile Thr Phe
 210 215 220

 His Gly Glu Gly Asp Gln Glu Pro Gly Leu Glu Pro Gly Asp Ile Ile
 225 230 235 240

 Ile Val Leu Asp Gln Lys Asp His Ala Val Phe Thr Arg Arg Gly Glu
 245 250 255

 Asp Leu Phe Met Cys Met Asp Ile Gln Leu Val Glu Ala Leu Cys Gly
 260 265 270

 Phe Gln Lys Pro Ile Ser Thr Leu Asp Asn Arg Thr Ile Val Ile Thr
 275 280 285

 Ser His Pro Gly Gln Ile Val Lys His Gly Asp Ile Lys Cys Val Leu
 290 295 300

 Asn Glu Gly Met Pro Ile Tyr Arg Arg Pro Tyr Glu Lys Gly Arg Leu
 305 310 315 320

 Ile Ile Glu Phe Lys Val Asn Phe Pro Glu Asn Gly Phe Leu Ser Pro
 325 330 335

 Asp Lys Leu Ser Leu Leu Glu Lys Leu Leu Pro Glu Arg Lys Glu Val
 340 345 350

 Glu Glu Thr Asp Glu Met Asp Gln Val Glu Leu Val Asp Phe Asp Pro
 355 360 365

 Asn Gln Glu Arg Arg Arg His Tyr Asn Gly Glu Ala Tyr Glu Asp Asp
 370 375 380

 Glu His His Pro Arg Gly Gly Val Gln Cys Gln Thr Ser
 385 390 395

 <210> 106
 <211> 340
 <212> PRT
 <213> Homo sapiens

 <400> 106
 Met Gly Lys Asp Tyr Tyr Gln Thr Leu Gly Leu Ala Arg Gly Ala Ser
 1 5 10 15

Asp Glu Glu Ile Lys Arg Ala Tyr Arg Arg Gln Ala Leu Arg Tyr His
 20 25 30

Pro Asp Lys Asn Lys Glu Pro Gly Ala Glu Glu Lys Phe Lys Glu Ile
 35 40 45

Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys Arg Glu Ile Phe
 50 55 60

Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser Gly Pro Ser Gly Gly
 65 70 75 80

Ser Gly Gly Gly Ala Asn Gly Thr Ser Phe Ser Tyr Thr Phe His Gly
 85 90 95

Asp Pro His Ala Met Phe Ala Glu Phe Phe Gly Gly Arg Asn Pro Phe
 100 105 110

Asp Thr Phe Phe Gly Gln Arg Asn Gly Glu Glu Gly Met Asp Ile Asp
 115 120 125

Asp Pro Phe Ser Gly Phe Pro Met Gly Met Gly Gly Phe Thr Asn Val
 130 135 140

Asn Phe Gly Arg Ser Arg Ser Ala Gln Glu Pro Ala Arg Lys Lys Gln
 145 150 155 160

Asp Pro Pro Val Thr His Asp Leu Arg Val Ser Leu Glu Glu Ile Tyr
 165 170 175

Ser Gly Cys Thr Lys Lys Met Lys Ile Ser His Lys Arg Leu Asn Pro
 180 185 190

Asp Gly Lys Ser Ile Arg Asn Glu Asp Lys Ile Leu Thr Ile Glu Val
 195 200 205

Lys Lys Gly Trp Lys Glu Gly Thr Lys Ile Thr Phe Pro Lys Glu Gly
 210 215 220

Asp Gln Thr Ser Asn Asn Ile Pro Ala Asp Ile Val Phe Val Leu Lys
 225 230 235 240

Asp Lys Pro His Asn Ile Phe Lys Arg Asp Gly Ser Asp Val Ile Tyr
 245 250 255

Pro Ala Arg Ile Ser Leu Arg Glu Ala Leu Cys Gly Cys Thr Val Asn
 260 265 270

Val Pro Thr Leu Asp Gly Arg Thr Ile Pro Val Val Phe Lys Asp Val
 275 280 285

Ile Arg Pro Gly Met Arg Arg Lys Val Pro Gly Glu Gly Leu Pro Leu
 290 295 300

Pro Lys Thr Pro Glu Lys Arg Gly Asp Leu Ile Ile Glu Phe Glu Val
 305 310 315 320
 Ile Phe Pro Glu Arg Ile Pro Gln Thr Ser Arg Thr Val Leu Glu Gln
 325 330 335
 Val Leu Pro Ile
 340

<210> 107
 <211> 351
 <212> PRT
 <213> Homo sapiens

<400> 107
 Met Ala Ser Tyr Tyr Glu Ile Leu Asp Val Pro Arg Ser Ala Ser Ala
 1 5 10 15

Asp Asp Ile Lys Lys Ala Tyr Arg Arg Lys Ala Leu Gln Trp His Pro
 20 25 30

Asp Lys Asn Pro Asp Asn Lys Glu Phe Ala Glu Lys Lys Phe Lys Glu
 35 40 45

Val Ala Glu Ala Tyr Glu Val Leu Ser Asp Lys His Lys Arg Glu Ile
 50 55 60

Tyr Asp Arg Tyr Gly Arg Glu Gly Leu Thr Gly Thr Gly Thr Gly Pro
 65 70 75 80

Ser Arg Ala Glu Ala Gly Ser Gly Gly Pro Gly Phe Thr Phe Thr Phe
 85 90 95

Arg Ser Pro Glu Glu Val Phe Arg Glu Phe Phe Gly Ser Gly Asp Pro
 100 105 110

Phe Ala Glu Leu Phe Asp Asp Leu Gly Pro Phe Ser Glu Leu Gln Asn
 115 120 125

Arg Gly Ser Arg His Ser Gly Pro Phe Phe Thr Phe Ser Ser Ser Phe
 130 135 140

Pro Gly His Ser Asp Phe Ser Ser Ser Phe Ser Phe Ser Pro Gly
 145 150 155 160

Ala Gly Ala Phe Arg Ser Val Ser Thr Ser Thr Thr Phe Val Gln Gly
 165 170 175

Arg Arg Ile Thr Thr Arg Arg Ile Met Glu Asn Gly Gln Glu Arg Val
 180 185 190

Glu Val Glu Glu Asp Gly Gln Leu Lys Ser Val Thr Ile Asn Gly Val
 195 200 205

Pro Asp Asp Leu Ala Arg Gly Leu Glu Leu Ser Arg Arg Glu Gln Gln
 210 215 220
 Pro Ser Val Thr Ser Arg Ser Gly Gly Thr Gln Val Gln Gln Thr Pro
 225 230 235 240
 Ala Ser Cys Pro Leu Asp Ser Asp Leu Ser Glu Asp Glu Asp Leu Gln
 245 250 255
 Leu Ala Met Ala Tyr Ser Leu Ser Glu Met Glu Ala Ala Gly Lys Lys
 260 265 270
 Pro Ala Gly Gly Arg Glu Ala Gln His Arg Arg Gln Gly Arg Pro Arg
 275 280 285
 Pro Ser Thr Lys Ile Gln Ala Trp Gly Gly Pro Arg Arg Val Arg Gly
 290 295 300
 Val Lys Gln Pro Asn Ala Val His Pro Gln Arg Arg Arg Pro Leu Ala
 305 310 315 320
 Ala Ser Ser Ser Glu His Arg Ala Gln Pro Asp Leu Ile Gln Ile Leu
 325 330 335
 Thr Gly Gly Ser Asp Ser Leu Trp Glu Glu Lys Arg Gly Val Ser
 340 345 350

 <210> 108
 <211> 848
 <212> DNA
 <213> Mus musculus

 <220>
 <221> CDS
 <222> (30) .. (764)

 <400> 108
 caaggagcct ctgcctgccc gtcgtcgtc atg ccg tcc ctg ttg ctc cag ctg 53
 Met Pro Ser Leu Leu Leu Gln Leu
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 ccc ctg cgc cta tgc cgg ctg tgg ccg cat agc ctt tcc atc cga ctt 101

 Pro Leu Arg Leu Cys Arg Leu Trp Pro His Ser Leu Ser Ile Arg Leu
 10 15 20

 ctc aca gcc gcc aca ggg cag cgg tct gtc cct act aat tac tat gaa 149

 Leu Thr Ala Ala Thr Gly Gln Arg Ser Val Pro Thr Asn Tyr Tyr Glu
 25 30 35 40

 ttg ttg ggc gtg cat ccg ggt gcc agc gct gaa gag att aaa cgt gct 197

Leu	Leu	Gly	Val	His	Pro	Gly	Ala	Ser	Ala	Glu	Glu	Ile	Lys	Arg	Ala	
				45						50					55	
ttt ttc acc aag tca aaa gag cta cac cct gat cga gac cct ggg aac															245	
Phe	Phe	Thr	Lys	Ser	Lys	Glu	Leu	His	Pro	Asp	Arg	Asp	Pro	Gly	Asn	
			60					65					70			
cca gcc ctg cat agc cgc ttt gtg gag ctg aat gag gca tat cga gtg															293	
Pro	Ala	Leu	His	Ser	Arg	Phe	Val	Glu	Leu	Asn	Glu	Ala	Tyr	Arg	Val	
	75				80					85						
ctc agt cgt gag gaa agt cgt cgt aac tat gac cac cag ctg cat tca															341	
Leu	Ser	Arg	Glu	Glu	Ser	Arg	Arg	Asn	Tyr	Asp	His	Gln	Leu	His	Ser	
	90				95					100						
gcc agt cct cca aag tct tca ggg agc aca gcc gag cct aag tat acg															389	
Ala	Ser	Pro	Pro	Lys	Ser	Ser	Gly	Ser	Thr	Ala	Glu	Pro	Lys	Tyr	Thr	
105				110					115			120				
caa cag aca cac agc agc tcc tgg gaa ccc ccc aac gct caa tac tgg															437	
Gln	Gln	Thr	His	Ser	Ser	Ser	Trp	Glu	Pro	Pro	Asn	Ala	Gln	Tyr	Trp	
			125				130			135						
gcc cag ttc cac agt gtg agg ccg cag ggg ccg gag tca agg aag cag															485	
Ala	Gln	Phe	His	Ser	Val	Arg	Pro	Gln	Gly	Pro	Glu	Ser	Arg	Lys	Gln	
	140				145						150					
cag cgt aaa cac aac cag cgg gtc ctg ggg tac tgc ctc ctg ctc atg															533	
Gln	Arg	Lys	His	Asn	Gln	Arg	Val	Leu	Gly	Tyr	Cys	Leu	Leu	Met		
	155				160						165					
gtg gca ggc atg ggc ctg cac tat gtt gcc ttc agg aag ctg gag cag															581	
Val	Ala	Gly	Met	Gly	Leu	His	Tyr	Val	Ala	Phe	Arg	Lys	Leu	Glu	Gln	
	170				175					180						
gtg cat cgc agc ttc atg gat gaa aag gac cgg atc att aca gcc atc															629	
Val	His	Arg	Ser	Phe	Met	Asp	Glu	Lys	Asp	Arg	Ile	Ile	Thr	Ala	Ile	
185				190				195			200					
tac aat gac act cgg gcc agg gcc agg gcc aac aga gcc agg att cag															677	
Tyr	Asn	Asp	Thr	Arg	Ala	Arg	Ala	Arg	Ala	Asn	Arg	Ala	Arg	Ile	Gln	
	205				210					215						
cag gag cgc cac gag agg cag cag cgg gca gaa ccc tcc ctg cct															725	

Gln Glu Arg His Glu Arg Gln Gln Pro Arg Ala Glu Pro Ser Leu Pro
 220 225 230
 cca gaa agc tcc agg atc atg ccc cag gac aca agc ccc tgagaggctt 774
 Pro Glu Ser Ser Arg Ile Met Pro Gln Asp Thr Ser Pro
 235 240 245
 aactaaatgg gaccttcatt ggtcctctcc ctgctgcctg tccagaacta cacgtgcaat 834
 aaactcattt tcag 848

 <210> 109
 <211> 245
 <212> PRT
 <213> Mus musculus

 <400> 109
 Met Pro Ser Leu Leu Leu Gln Leu Pro Leu Arg Leu Cys Arg Leu Trp
 1 5 10 15
 Pro His Ser Leu Ser Ile Arg Leu Leu Thr Ala Ala Thr Gly Gln Arg
 20 25 30
 Ser Val Pro Thr Asn Tyr Tyr Glu Leu Leu Gly Val His Pro Gly Ala
 35 40 45
 Ser Ala Glu Glu Ile Lys Arg Ala Phe Phe Thr Lys Ser Lys Glu Leu
 50 55 60
 His Pro Asp Arg Asp Pro Gly Asn Pro Ala Leu His Ser Arg Phe Val
 65 70 75 80
 Glu Leu Asn Glu Ala Tyr Arg Val Leu Ser Arg Glu Glu Ser Arg Arg
 85 90 95
 Asn Tyr Asp His Gln Leu His Ser Ala Ser Pro Pro Lys Ser Ser Gly
 100 105 110
 Ser Thr Ala Glu Pro Lys Tyr Thr Gln Gln Thr His Ser Ser Ser Trp
 115 120 125
 Glu Pro Pro Asn Ala Gln Tyr Trp Ala Gln Phe His Ser Val Arg Pro
 130 135 140
 Gln Gly Pro Glu Ser Arg Lys Gln Gln Arg Lys His Asn Gln Arg Val
 145 150 155 160
 Leu Gly Tyr Cys Leu Leu Leu Met Val Ala Gly Met Gly Leu His Tyr
 165 170 175
 Val Ala Phe Arg Lys Leu Glu Gln Val His Arg Ser Phe Met Asp Glu
 180 185 190

Lys Asp Arg Ile Ile Thr Ala Ile Tyr Asn Asp Thr Arg Ala Arg Ala
195 200 205

Arg Ala Asn Arg Ala Arg Ile Gln Gln Glu Arg His Glu Arg Gln Gln
210 215 220

Pro Arg Ala Glu Pro Ser Leu Pro Pro Glu Ser Ser Arg Ile Met Pro
225 230 235 240

Gln Asp Thr Ser Pro
245

<210> 110

<211> 120

<212> DNA

<213> Homo sapiens

<400> 110

ttgaagtcta gccccatcct ggtccaatgc gctcttgta gcctccttcc ccagctgccc 60

gccccggcc atgccggccct tactggccct gcgcctgtg ccggctgtgg ccccgcaaccc 120

<210> 111

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: The amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:20.

<400> 111

Glu Phe Gly Thr Ser
1 5